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FIG. 1A

Figure 1B: Sequence alignment of MOR, DOR, SOM1, and SOM2.

MOR	WENLIKICVFIIFAFIMPILLITVCYGLMILRLKSVRMLSGSKEKDRLNRR	277
DOR	-DTVT-----VV-----L----R----L-----S---	258
SOM1	-LVGFVLYT-LMG-LI-VGA-CL--V-I-AKMRM-WQQRK-SE-K	268
SOM2	-YTGFRI-YA--LG-LV-LT--CL--LRI-IKV--SGIRV--SKRKKSEKK	253
V		
MOR	ITRMVLLVVVAWFIVCWTPIHIYYVIKALITIPETFQTV SWHFCIALGY	326
DOR	-----GA-V---A---F---VWT-VD-NRRDPLV-AAL-L-----	308
SOM1	--L--MM--M--VI--M--FYVV Q--VNVEAEDDATV-QLSV-----	313
SOM2	V---SI-----F--L-FY-FNVSSVSSVA-SP-PALKGMFDVVV--T-	302
VI		
MOR	TNSCLNPVLYAFLDENFKRCFREFCIPTSSSTIEQQNSTRVRQ NTREHPS	375
DOR	A--S-----QL-RTPCGRQ-PGSLR-P--AT--RV	357
SOM1	A---A--I--G--SD----S-QRILCLSMWDNAEEPVDDY ATALKSRA	362
SOM2	A---A--I--A--SD---KS-QNVLCLVKVSGAEDGERSDSKQDKSRLNE	352
VII		
MOR	TANTVDRTNHOLEAEТАPLP	398
DOR	--C- PSDGPGGAAA	372
SOM1	YSVEDFOOPENILESGGVFRNGTCASRISTL	391
SOM2	-TE- Q--LLNGDLQTSI	369

FIG. 1B

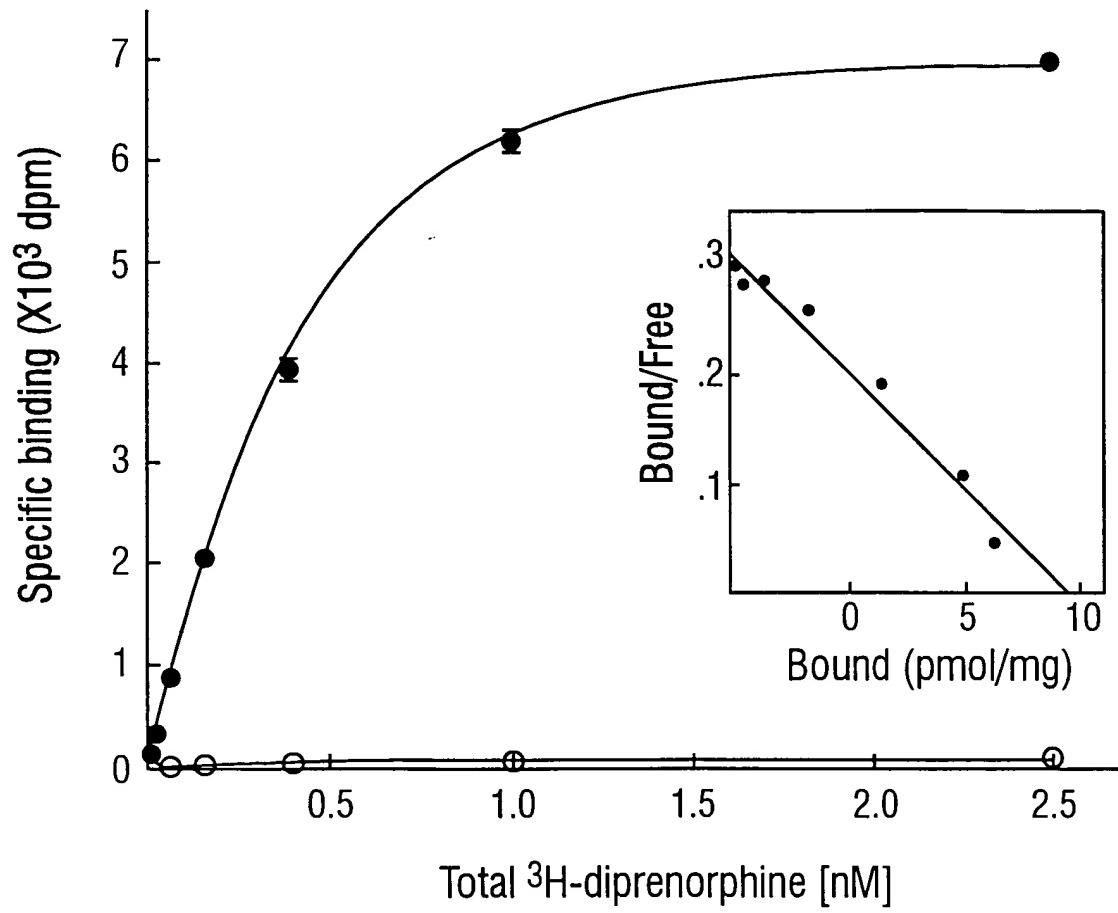


FIG.2

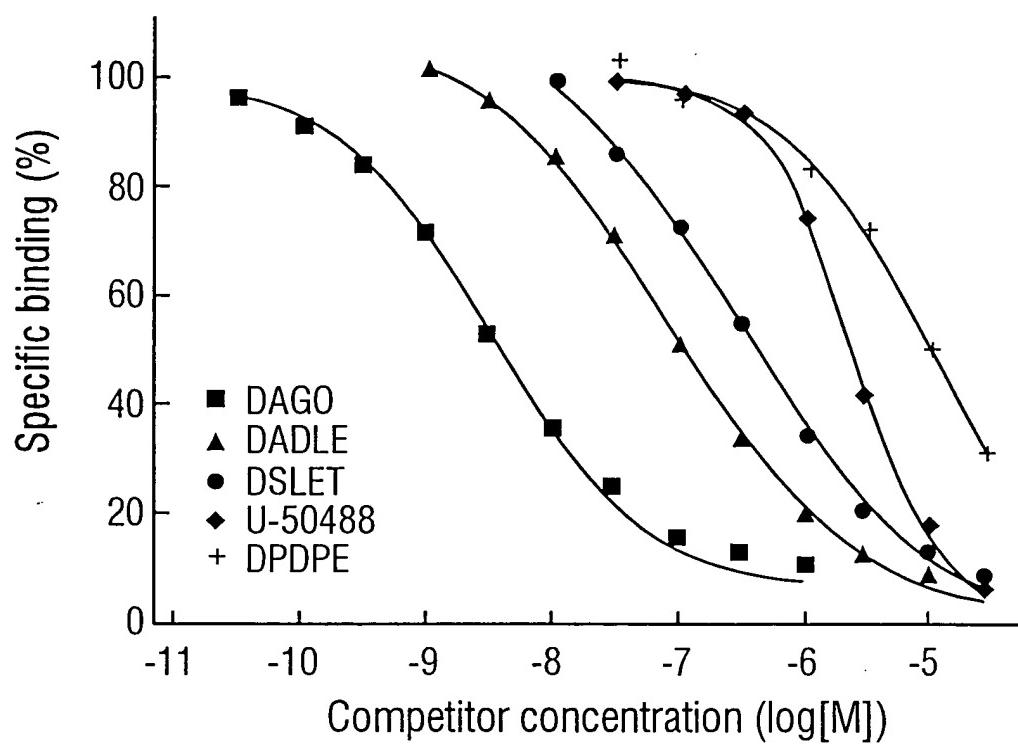


FIG. 3A

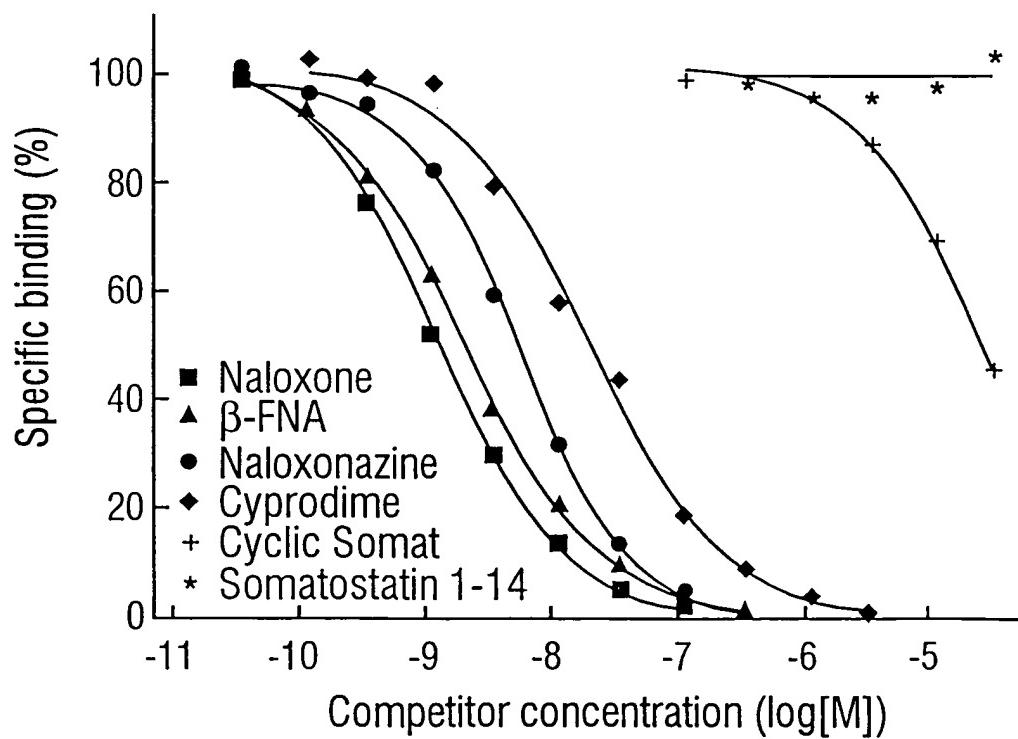


FIG. 3B

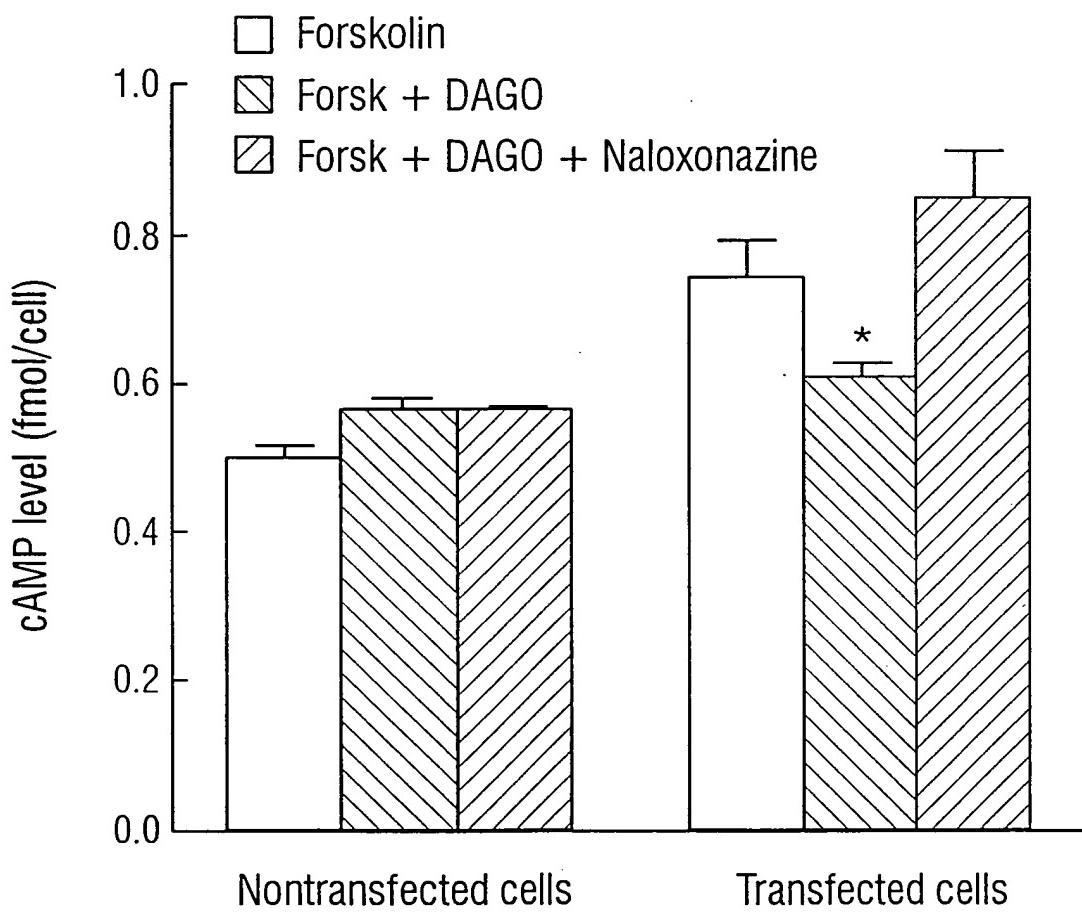


FIG. 4